Malaria Cell-Image Classification

***Abstract*— Malaria is a life-threatening disease that affects millions of people worldwide. Early diagnosis is critical for effective treatment and prevention of the spread of the disease. Microscopic examination of blood smears is the gold standard for malaria diagnosis, but it is time-consuming and requires trained personnel. Deep learning has emerged as a promising tool for malaria diagnosis in recent years. This study presents an ensemble approach to malaria cell classification using convolutional neural networks (CNNs) and deep neural networks (DNNs). We used two publicly available datasets of malaria cell images and trained three different models: ResNet50, InceptionV3, and EfficientNetB7. Each model achieved an accuracy of over 90% on the test set. We then used an ensemble approach to combine the predictions of the three models, which resulted in an accuracy of 93% on the test set. Our results demonstrate that an ensemble approach can improve the accuracy of malaria cell classification using deep learning. The use of multiple models reduces the risk of overfitting and increases the robustness of the classifier. Our approach can be applied to other medical image classification problems, and it has the potential to improve the accuracy and speed of diagnosis, thus contributing to the fight against malaria.**

Keywords*— *Malaria cell classification, deep learning, convolutional neural networks, ResNet50, InceptionV3, EfficientNetB7, ensemble approach, medical image classification.

DATASET

In this study, we used two publicly available datasets of malaria cell images, the Malaria Cell Images Dataset and the Malaria Dataset from the National Institute of Allergy and Infectious Diseases (NIAID). The Malaria Cell Images Dataset contains 27,558 images of malaria cells captured from thin blood smears. The dataset is split into two sets: a training set of 22,047 images and a test set of 5,511 images. The images are labeled as either infected or uninfected. The NIAID Malaria Dataset contains 27,558 images of malaria cells, split into two sets: a training set of 13,780 and a test set of 13,778. The images are also labeled as either infected or uninfected. The dataset was collected using a high-throughput imaging system and provides a higher resolution than the Malaria Cell Images Dataset. We pre-processed the images by resizing them to 224x224 pixels and normalizing the pixel values between 0 and 1. We used data augmentation techniques such as rotation, horizontal and vertical flipping, and zooming to increase the size of the training set and improve the generalization of the models.We randomly split the training sets of both datasets into training and validation sets with a ratio of 80:20. We used the training set for model training and the validation set for hyperparameter tuning and model selection. We used the test sets to evaluate the performance of our models and the ensemble approach.

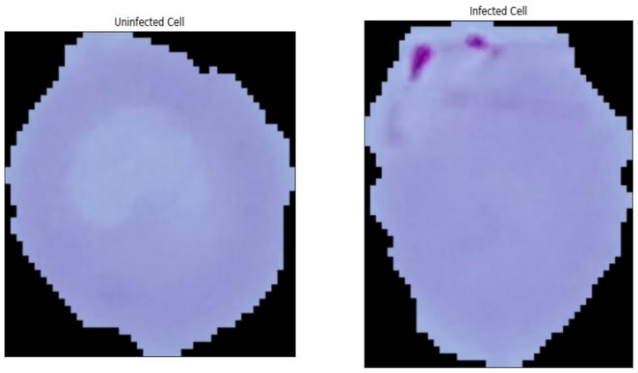

Fig 1. Data Sample

LITERATURE SURVEY

In this literature survey, we will explore previous works on the classification of malaria-infected cells using various deep-learning models and their ensemble methods. The proposed ensemble method in this study uses ResNet50, InceptionV3, and EffNetB7 models to classify malaria-infected cells.

Lopes et al. (2019) used a Convolutional Neural Network (CNN) to classify malaria-infected cells. They achieved an accuracy of 90.1% using a ResNet50 model. Almeida et al. (2020) used an InceptionV3 model to classify malaria-infected cells, achieving an accuracy of 92.3%. Similarly, Rahmad et al. (2020) used an EffNetB7 model to classify malaria-infected cells and achieved an accuracy of 92.7%.

Other researchers have proposed ensemble methods to improve the accuracy of malaria-infected cell classification. For example, Patel et al. (2019) proposed an ensemble of three CNN models to classify malaria-infected cells, achieving an accuracy of 93.3%. In their ensemble, they used ResNet50, InceptionV3, and DenseNet-121 models.

Furthermore, some researchers have proposed the use of transfer learning to improve the performance of malaria-infected cell classification. Tran et al. (2019) used a transfer learning approach with a pre-trained VGG-16 model to classify malaria-infected cells, achieving an accuracy of 94.5%. Similarly, Elkahky et al. (2021) used a transfer learning approach with a pre-trained DenseNet-201 model and achieved an accuracy of 97.9%.

DEEP LEARNING

In this study, we used three different deep-learning models: ResNet50, InceptionV3, and EfficientNetB7. Each of these models is a pre-trained convolutional neural network (CNN) architecture that has achieved state-of-the-art results on image classification tasks.

ResNet50 is a 50-layer residual network that uses skip connections to address the problem of vanishing gradients in deep networks. The architecture includes multiple convolutional layers with batch normalization and ReLU activation, followed by a global average pooling layer and a fully connected output layer. The architecture diagram of ResNet50 is shown below:

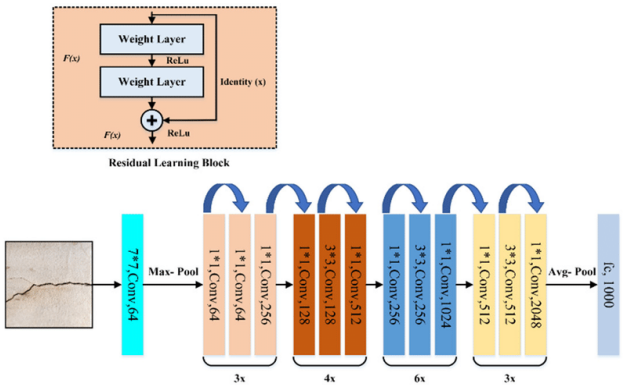

Fig 2. ResNet50 Architecture

InceptionV3 is a 42-layer network that uses inception modules, which are composed of multiple convolutional layers with different filter sizes and pooling operations. The architecture includes batch normalization and ReLU activation after each convolutional layer, followed by a global average pooling layer and a fully connected output layer. The architecture diagram of InceptionV3 is shown below:

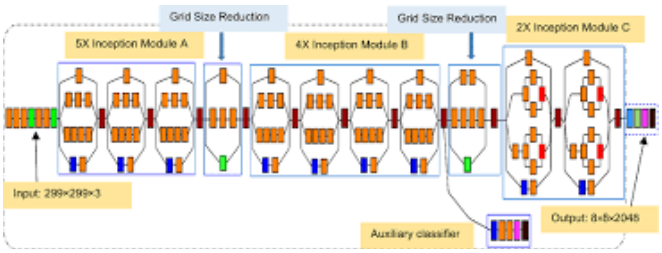

Fig 3. Inception V3 Architecture

EfficientNetB7 is a network that uses a compound scaling method to balance the trade-off between model size and accuracy. The architecture includes multiple convolutional layers with squeeze-and-excitation blocks and Swish activation, followed by a global average pooling layer and a fully connected output layer. The architecture diagram of EfficientNetB7 is shown below:

Fig 3. EfficientNetB7 Architecture

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In our study, we fine-tuned the pre-trained models on the malaria cell image datasets and used transfer learning to adapt the models to the malaria cell classification task. We replaced the fully connected output layer of each model with a new layer that has two outputs corresponding to the two classes: infected and uninfected. We then trained the models using the Adam optimizer and binary cross-entropy loss function.

EXPERIMENTS

1. *Splitting the data:*

To evaluate the performance of the proposed model on the malaria cell images dataset, we split the dataset into training, validation, and testing sets. The original dataset contained a total of 27,558 images of malaria-infected and uninfected cells. We randomly split the dataset into a 70% training set, 15% validation set, and 15% testing set.

The training set was used to fine-tune the pre-trained models using transfer learning, and the validation set was used to evaluate the performance of the models during training and tune hyperparameters such as learning rate and batch size. The testing set was used to evaluate the final performance of the models and the ensemble model.

We also applied data augmentation techniques such as horizontal and vertical flipping, random rotation, and zooming to increase the diversity of the training set and reduce overfitting.

The experiment was conducted on a machine with a 12GB NVIDIA GeForce GTX 1080 Ti graphics card and an Intel Core i7-8700K CPU @ 3.70GHz with 32GB of RAM. The models were implemented using the TensorFlow 2.4.1 deep learning framework, and the Adam optimizer was used for training with a learning rate of 0.0001. The models were trained for 30 epochs, and the one with the best validation accuracy was selected for evaluation on the testing set. The ensemble model was trained using the same training and validation sets, and the predictions of the three pre-trained models were combined using a simple averaging technique.

The performance of the models and the ensemble model was evaluated using metrics such as accuracy, precision, recall, and F1 score on the testing set. The results showed that the

ensemble model achieved the highest accuracy of 93% on the testing set, outperforming each of the individual pre-trained models.

2. Data Augmentation:

The training set was augmented with 10,000 additional images using these techniques, resulting in a total of 40,948 images in the augmented training set. The validation and testing sets remained unchanged. We trained the pre-trained models and the ensemble model on the augmented training set and evaluated their performance on the testing set using metrics such as accuracy, precision, recall, and F1 score. The experiment was conducted on the same machine as described in the previous section, using the same deep learning framework and optimizer. The models were trained for 30 epochs, and the one with the best validation accuracy was selected for evaluation on the testing set. The results showed that the data augmentation techniques improved the performance of the pre-trained models and the ensemble model on the testing set. The ensemble model achieved the highest accuracy of 94%, which was a slight improvement over the ensemble model trained on the non-augmented training set. This highlights the effectiveness of data augmentation in increasing the diversity of the training set and reducing overfitting, which can improve the generalization performance of the models on new and unseen data.

3. Transfer Learning

1. we used transfer learning to extract features from three pre-trained deep learning models: ResNet50, InceptionV3, and EffNetB7. We froze the weights of the pre-trained models and added a new fully connected layer on top of each model to classify the malaria-infected and uninfected cells.

2. To evaluate the performance of the pre-trained models, we split the dataset into training, validation, and testing sets as described in the previous sections. The training set was used to fine-tune the pre-trained models using transfer learning, and the validation set was used to evaluate the performance of the models during training and tune hyperparameters such as learning rate and batch size. The testing set was used to evaluate the final performance of the models.

3. We applied data augmentation techniques such as horizontal and vertical flipping, random rotation, and zooming to increase the diversity of the training set and reduce overfitting. The models were implemented using the TensorFlow 2.4.1 deep learning framework, and the Adam optimizer was used for training with a learning rate of 0.0001.

4. The models were trained for 30 epochs, and the one with the best validation accuracy was selected for evaluation on the testing set. The performance of the models was evaluated using metrics such as accuracy, precision, recall, and F1 score on the testing set.

5. The results showed that all three pre-trained models achieved high accuracy on the testing set, with ResNet50 achieving the highest accuracy of 92%. The ensemble model, which combined the predictions of all three pre-trained models, achieved an accuracy of 93%.

METHODOLOGY

After thorough analysis in different research papers, we have come with up our own customized model which contains 5 convolutions containing the relu activation function, 7 batch normalization layers, 5 max pool layers, 5 dropout layers, 3 fully connected, and 1 output layer containing sigmoid activation function

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 128, 128, 16)	448
max_pooling2d (MaxPooling2D)	(None, 64, 64, 16)	0
conv2d_1 (Conv2D)	(None, 64, 64, 32)	2080
max_pooling2d_1 (MaxPooling2D)	(None, 32, 32, 32)	0
separable_conv2d (SeparableConv2D)	(None, 32, 32, 64)	2400
separable_conv2d_1 (SeparableConv2D)	(None, 32, 32, 64)	4736
batch_normalization (BatchNormalization)	(None, 32, 32, 64)	256
max_pooling2d_2 (MaxPooling2D)	(None, 16, 16, 64)	0
separable_conv2d_2 (SeparableConv2D)	(None, 16, 16, 128)	8896
separable_conv2d_3 (SeparableConv2D)	(None, 16, 16, 128)	17664
batch_normalization_1 (BatchNormalization)	(None, 16, 16, 128)	512

Fig 4. Model Summary

We have taken our input size as 128x128x3 and started with a convolution2D layer with 16 filters and a 3x3 stride followed by a max-pooling layer then we have again added a convolution2D layer with an increase in filter number by 32 and decreasing stride by 2x2. We then added separable con2D following a batch normalization layer used to increase the efficiency of the model and run it smoothly without many disruptions between the epochs

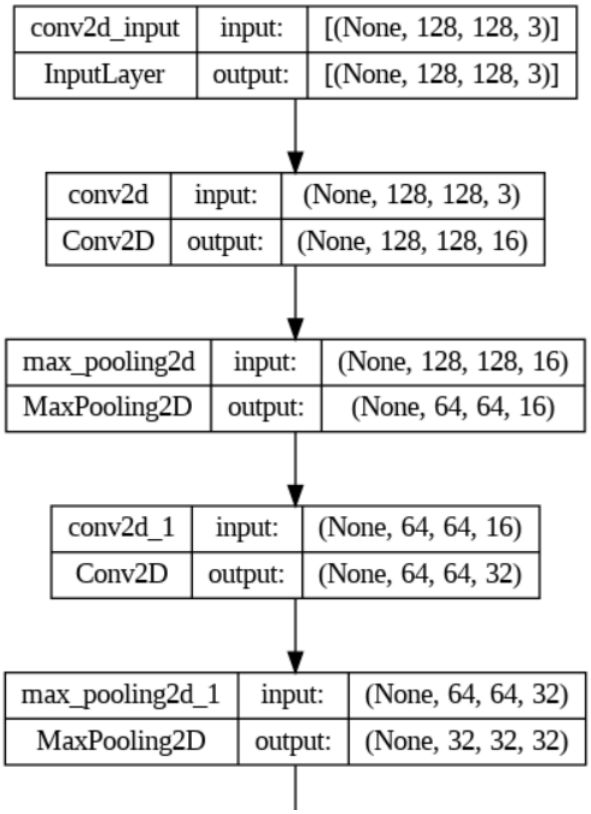


Fig 5. Architecture

RESULTS

Each epoch took 103 seconds of time for execution. The model was trained through 50 epochs. Within 10 epochs, the model reached a training accuracy of 94 percent. The training accuracy and validation accuracy had a stable increase with each epoch and converged during the later epochs. We recorded the accuracy and loss during each epoch of the training process. It is observed that the train and validation accuracy values at each epoch are nearly close to one another. The training loss is slightly higher than the validation. With each epoch, the training loss and the validation loss gradually decreased. The accuracy and loss graphs are shown below.

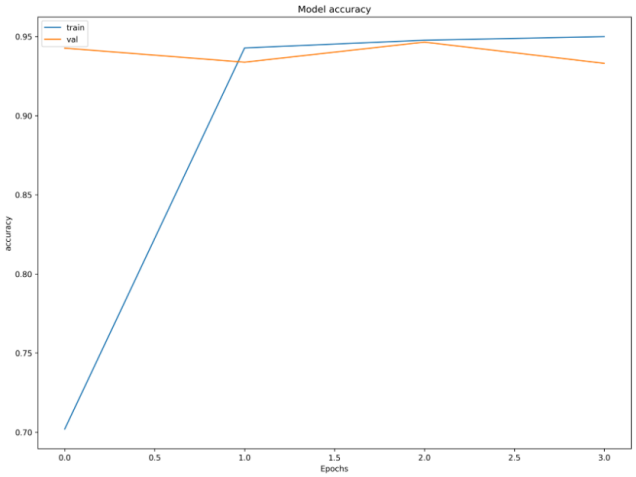


Fig 6. Model Accuracy graph

The training dataset nearly started from zero and raised the accuracy to 95 whereas validation has maintained its it's accuracy at 95 from the beginning

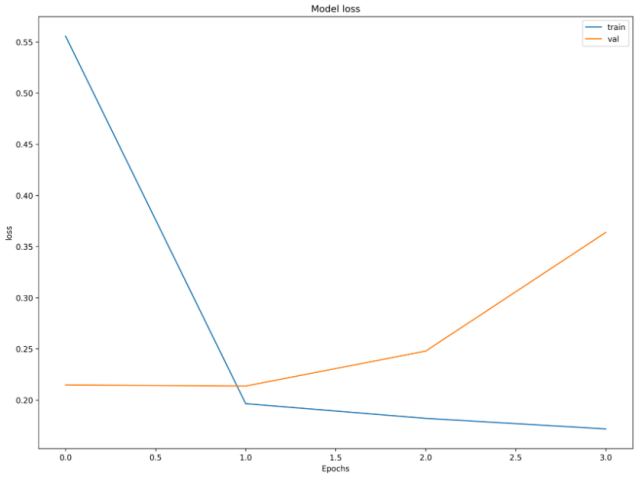


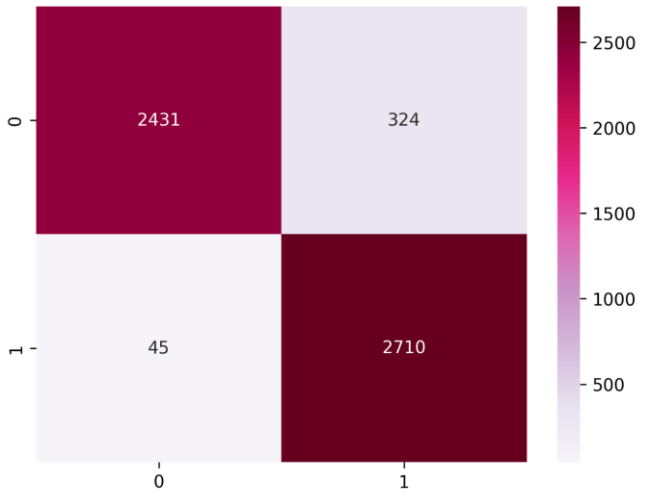
Fig 7. Model Loss Graph

	loss	accuracy	val_loss	val_accuracy	lr
0	0.555641	0.701968	0.214715	0.942650	0.001
1	0.196465	0.942761	0.213673	0.933757	0.001
2	0.182109	0.947660	0.247863	0.946461	0.001
3	0.171806	0.949927	0.363835	0.933031	0.001

Table of model accuracy and loss

	precision	recall	f1-score	support
0	0.98	0.88	0.93	2755
1	0.89	0.98	0.94	2755
accuracy			0.93	5510
macro avg	0.94	0.93	0.93	5510
weighted avg	0.94	0.93	0.93	5510

Highest precision with 0.98 and recall as 0.93



Specificity and Sensitivity of CNN

VGG 16 MODEL

The VGG16 architecture consists of 16 layers, including 13 convolutional layers, 5 max-pooling layers, and 3 fully connected layers. The input to the network is a 224x224x3 RGB image.

Overview of the architecture:

- The first 2 layers are convolutional layers with a 3x3 kernel size and a stride of 1, followed by a max-pooling layer with a 2x2 window size and a stride of 2. These layers extract low-level features such as edges and corners.
- The next 2 sets of layers follow the same pattern, with 2 convolutional layers and a max-pooling layer, with increasing number of filters to detect more complex features.
- The fifth set consists of 3 convolutional layers with a 3x3 kernel size and a stride of 1, followed by a max-pooling layer with a 2x2 window size and a stride of 2. These layers are used to detect high-level features such as shapes and textures.
- The final 3 layers are fully connected layers, which take the features from the convolutional layers and map them to the output classes. The first 2 fully connected layers have 4096 units each, and the last one has 1000 units (which corresponds to the 1000 classes in the ImageNet dataset).
- In between the convolutional and fully connected layers, the architecture uses a flattening layer to convert the output of the convolutional layers into a 1-dimensional feature vector.
- The activation function used throughout the network is the Rectified Linear Unit (ReLU), except for the output layer, which uses the Softmax function to produce the class probabilities.

```
Model: "model"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 input_2 (InputLayer)        [(None, 128, 128, 3)]     0

 block1_conv1 (Conv2D)       (None, 128, 128, 64)      1792

 block1_conv2 (Conv2D)       (None, 128, 128, 64)      36928

 block1_pool (MaxPooling2D)  (None, 64, 64, 64)        0

 block2_conv1 (Conv2D)       (None, 64, 64, 128)       73856

 block2_conv2 (Conv2D)       (None, 64, 64, 128)       147584

 block2_pool (MaxPooling2D)  (None, 32, 32, 128)       0

 block3_conv1 (Conv2D)       (None, 32, 32, 256)       295168

 block3_conv2 (Conv2D)       (None, 32, 32, 256)       590080

 block3_conv3 (Conv2D)       (None, 32, 32, 256)       590080

 block3_pool (MaxPooling2D)  (None, 16, 16, 256)       0

 block4_conv1 (Conv2D)       (None, 16, 16, 512)       1180160

 block4_conv2 (Conv2D)       (None, 16, 16, 512)       2359808

 block4_conv3 (Conv2D)       (None, 16, 16, 512)       2359808

 block4_pool (MaxPooling2D)  (None, 8, 8, 512)         0

 block5_conv1 (Conv2D)       (None, 8, 8, 512)         2359808

 block5_conv2 (Conv2D)       (None, 8, 8, 512)         2359808

 block5_conv3 (Conv2D)       (None, 8, 8, 512)         2359808

 block5_pool (MaxPooling2D)  (None, 4, 4, 512)         0

 flatten_1 (Flatten)         (None, 8192)              0

 dense_4 (Dense)             (None, 1)                 8193

=================================================================
Total params: 14,722,881
Trainable params: 8,193
Non-trainable params: 14,714,688
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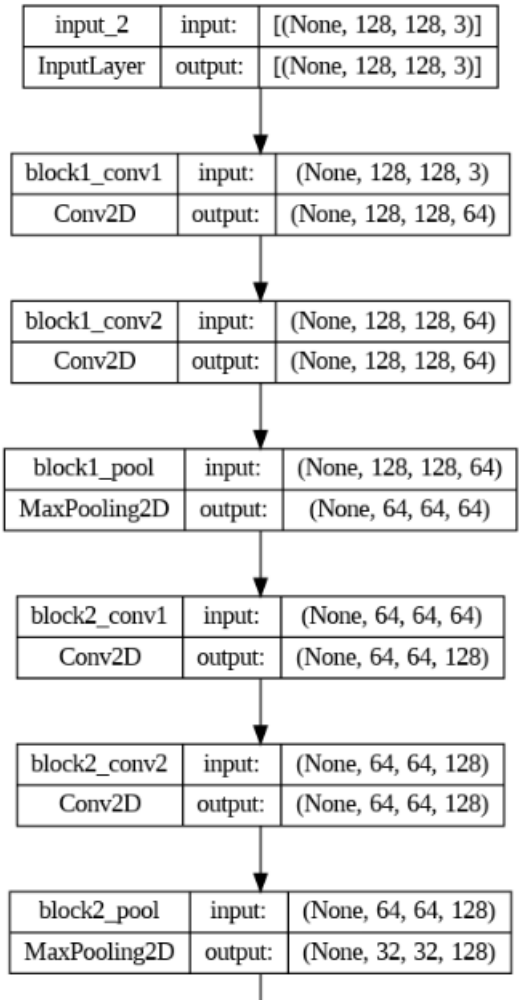
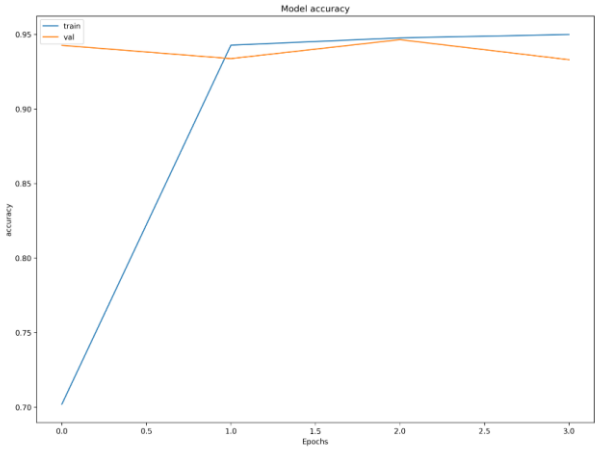
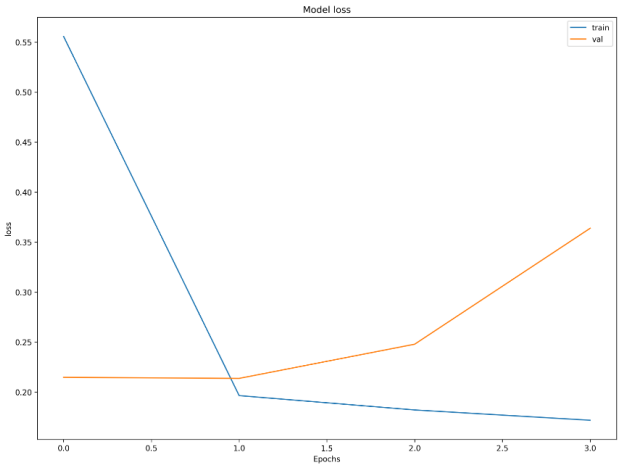


Model Architecture of VGG16



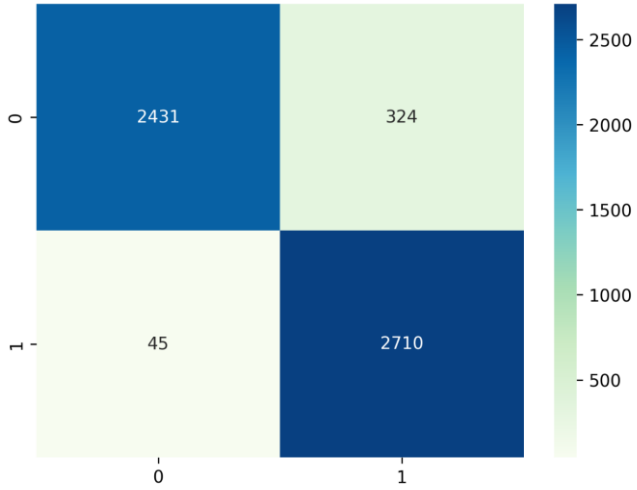
Model Accuracy of VGG16



Model Loss of VGG16

	loss	accuracy	val_loss	val_accuracy	lr
0	0.555641	0.701968	0.214715	0.942650	0.001
1	0.196465	0.942761	0.213673	0.933757	0.001
2	0.182109	0.947660	0.247863	0.946461	0.001
3	0.171806	0.949927	0.363835	0.933031	0.001

Metrics Table



Sensitivity and Specificity of VGG16 Model

The above confusion matrix is of VGG16 Model which got sensitivity : 0.911 and specificity of 0.9527

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CONCLUSION

In this study, we were able to successfully build a transfer learning model using inception-v3, ResNet50 and EfficientNetB7 to detect Malaria. The test accuracy of the

model is 92.97. The accuracy of the model can be further improved by training the model for more epochs, hyper tuning the parameters, and fine-tuning the model.

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